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***AMENDMENTS TO THE CLAIMS***

Please amend the claims as indicated hereafter.

1. (Previously amended) A method of synthesizing an unstructured nucleic acid, the method comprising steps of:

providing a nucleic acid template strand including a first template sequence element and a second template sequence element that is substantially complementary to the first template sequence element;

providing a collection of nucleotides sufficient to synthesize a nucleic acid strand complementary to at least a portion of the template nucleic acid strand, which portion includes the first and second template sequence elements, the collection including at least a first complementary nucleotide that hybridizes with a first residue within the first sequence element on the template strand and a second complementary nucleotide that hybridizes with a second residue within the second sequence element on the template strand, wherein the first and second residues are complementary to one another but the first and second nucleotides have a reduced ability to form a stable hydrogen bonded base pair; and

contacting the template and the nucleotides with an RNA polymerase enzyme characterized by an ability to polymerize the nucleotides under conditions and for a time sufficient to synthesize an unstructured nucleic acid in which said first complementary nucleotide and said second complementary nucleotide of the unstructured nucleic acid do not form an intramolecular base pair.

2-9. (Canceled previously)

10.-18. (Canceled)

19-24. (Canceled previously)

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25. (Previously added) The method of claim 1, wherein said first residue within said first sequence element on the template strand is adenine and said second residue within said second sequence element on the template strand is thymidine;

and wherein said first complementary nucleotide is 2-thiothymidine 5'-triphosphate and said second complementary nucleotide is 2-amino-2'-deoxyadenosine 5'-triphosphate.

26. (Previously added) The method of claim 1, wherein said first residue within said first sequence element on the template strand is adenine and said second residue within said second sequence element on the template strand is uridine;

and wherein said first complementary nucleotide is 2-thiothymidine 5'-triphosphate and said second complementary nucleotide is 2-amino-2'-deoxyadenosine 5'-triphosphate.

27. (Previously added) The method of claim 1, wherein said first residue within the first sequence element on the template strand is guanine and said second residue within said second sequence element on the template strand is cytidine;

and wherein said first complementary nucleotide is 2'-deoxypyrrrolo-pyrimidine 5'-triphosphate and said second complementary nucleotide is 2'-deoxyinosine 5'-triphosphate.

28. (Previously added) The method of claim 1, wherein said first residue within said first sequence element on the template strand is inosine and said second residue within said second sequence element on the template strand is cytidine;

and wherein said first complementary nucleotide is 2-thio-2'-deoxycytidine 5'-triphosphate and said second complementary nucleotide is 2'-deoxyguanosine 5'-triphosphate.

29. (Previously added) The method of claim 1, wherein said first residue within said first sequence element on the template strand is adenine and said second residue within said second sequence element on the template strand is thymidine;

and wherein said first complementary nucleotide is 2-thiouridine 5'-triphosphate and said second complementary nucleotide is 2-aminoadenosine 5'-triphosphate.

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30. (Previously added) The method of claim 1, wherein said first residue within said first sequence element on the template strand is adenine and said second residue within said second sequence element on the template strand is uridine;

and wherein said first complementary nucleotide is 2-thiouridine 5'-triphosphate and said second complementary nucleotide is 2-aminoadenosine 5'-triphosphate.

31. (Previously added) The method of claim 1, wherein said first residue within the first sequence element on the template strand is guanidine and said second residue within said second sequence element on the template strand is cytidine;

and wherein said first complementary nucleotide is pyrrolo-pyrimidine 5'-triphosphate and said second complementary nucleotide is inosine 5'-triphosphate.

32. (Previously added) The method of claim 1, wherein said first residue within said first sequence element on the template strand is inosine and said second residue within said second sequence element on the template strand is cytidine;

and wherein said first complementary nucleotide is 2-thiocytidine 5'-triphosphate and said second complementary nucleotide is guanosine 5'-triphosphate.

33. (Previously added) The method of claim 1, wherein said unstructured nucleic acid is at least 40 nucleotides in length.

34. (Previously added) The method of claim 1, wherein said unstructured nucleic acid is at least 100 nucleotides in length.

35. (Previously added) The method of claim 1, wherein said unstructured nucleic acid is at least 500 nucleotides in length.